A#9

1653

```
             RAW SEQUENCE LISTING              DATE: 12/28/2000
             PATENT APPLICATION:  US/09/331,631A     TIME: 08:00:58

             Input Set  : A:\CULLN23SEQ.txt
             Output Set: N:\CRF3\12282000\I331631A.raw

       4 <110> APPLICANT: Manners, John M.
       5          Marcus, John Paul
       6          Goulter, Kenneth C.
       7          Green, Jodie L.
       9 <120> TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
      12 <130> FILE REFERENCE: CULLN23.001APC
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/331,631A
C--> 14 <141> CURRENT FILING DATE: 1999-06-21
      14 <150> PRIOR APPLICATION NUMBER: PCT/AU97/00874
      15 <151> PRIOR FILING DATE: 1997-12-22
      17 <150> PRIOR APPLICATION NUMBER: AU PO 4275
      18 <151> PRIOR FILING DATE: 1996-12-20
      20 <160> NUMBER OF SEQ ID NOS: 40
      22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
      24 <210> SEQ ID NO: 1
      25 <211> LENGTH: 666
      26 <212> TYPE: PRT
      27 <213> ORGANISM: Macadamia integrifolia
      29 <400> SEQUENCE: 1
      30 Met Ala Ile Asn Thr Ser Asn Leu Cys Ser Leu Leu Phe Leu Leu Ser
      31  1               5                  10                  15
      32 Leu Phe Leu Leu Ser Thr Thr Val Ser Leu Ala Glu Ser Glu Phe Asp
      33               20                  25                  30
      34 Arg Gln Glu Tyr Glu Glu Cys Lys Arg Gln Cys Met Gln Leu Glu Thr
      35               35                  40                  45
      36 Ser Gly Gln Met Arg Arg Cys Val Ser Gln Cys Asp Lys Arg Phe Glu
      37          50                  55                  60
      38 Glu Asp Ile Asp Trp Ser Lys Tyr Asp Asn Gln Glu Asp Pro Gln Thr
      39 65                  70                  75                  80
      40 Glu Cys Gln Gln Cys Gln Arg Arg Cys Arg Gln Gln Glu Ser Gly Pro
      41               85                  90                  95
      42 Arg Gln Gln Gln Tyr Cys Gln Arg Arg Cys Lys Glu Ile Cys Glu Glu
      43               100                 105                 110
      44 Glu Glu Glu Tyr Asn Arg Gln Arg Asp Pro Gln Gln Gln Tyr Glu Gln
      45               115                 120                 125
      46 Cys Gln Lys His Cys Gln Arg Arg Glu Thr Glu Pro Arg His Met Gln
      47          130                 135                 140
      48 Thr Cys Gln Gln Arg Cys Glu Arg Arg Tyr Glu Lys Glu Lys Arg Lys
      49 145                 150                 155                 160
      50 Gln Gln Lys Arg Tyr Glu Glu Gln Gln Arg Glu Asp Glu Glu Lys Tyr
      51               165                 170                 175
      52 Glu Glu Arg Met Lys Glu Glu Asp Asn Lys Arg Asp Pro Gln Gln Arg
      53               180                 185                 190
      54 Glu Tyr Glu Asp Cys Arg Arg Arg Cys Glu Gln Gln Glu Pro Arg Gln
      55          195                 200                 205
      56 Gln His Gln Cys Gln Leu Arg Cys Arg Glu Gln Gln Arg Gln His Gly
      57          210                 215                 220
```

RAW SEQUENCE LISTING   DATE: 12/28/2000
PATENT APPLICATION: US/09/331,631A   TIME: 08:00:58

Input Set : A:\CULLN23SEQ.txt
Output Set: N:\CRF3\12282000\I331631A.raw

```
58  Arg Gly Gly Asp Met Met Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr
59  225                 230                 235                 240
60  Glu Glu Gly Glu Glu Glu Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu
61                  245                 250                 255
62  Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val
63              260                 265                 270
64  Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn
65          275                 280                 285
66  Tyr Arg Leu Val Leu Leu Glu Ala Asn Pro Asn Ala Phe Val Leu Pro
67      290                 295                 300
68  Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Ile Gly Gly Arg Gly
69  305                 310                 315                 320
70  Ala Leu Lys Met Ile His His Asp Asn Arg Glu Ser Tyr Asn Leu Glu
71              325                 330                 335
72  Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile
73              340                 345                 350
74  Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr
75          355                 360                 365
76  Ile Ser Thr Pro Gly Gln Tyr Lys Glu Phe Phe Pro Ala Gly Gly Gln
77      370                 375                 380
78  Asn Pro Glu Pro Tyr Leu Ser Thr Phe Ser Lys Glu Ile Leu Glu Ala
79  385                 390                 395                 400
80  Ala Leu Asn Thr Gln Thr Glu Lys Leu Arg Gly Val Phe Gly Gln Gln
81              405                 410                 415
82  Arg Glu Gly Val Ile Ile Arg Ala Ser Gln Glu Gln Ile Arg Glu Leu
83              420                 425                 430
84  Thr Arg Asp Asp Ser Glu Ser Arg His Trp His Ile Arg Arg Gly Gly
85          435                 440                 445
86  Glu Ser Ser Arg Gly Pro Tyr Asn Leu Phe Asn Lys Arg Pro Leu Tyr
87      450                 455                 460
88  Ser Asn Lys Tyr Gly Gln Ala Tyr Glu Val Lys Pro Glu Asp Tyr Arg
89  465                 470                 475                 480
90  Gln Leu Gln Asp Met Asp Leu Ser Val Phe Ile Ala Asn Val Thr Gln
91              485                 490                 495
92  Gly Ser Met Met Gly Pro Phe Phe Asn Thr Arg Ser Thr Lys Val Val
93              500                 505                 510
94  Val Val Ala Ser Gly Glu Ala Asp Val Glu Met Ala Cys Pro His Leu
95              515                 520                 525
96  Ser Gly Arg His Gly Gly Arg Gly Gly Lys Arg His Glu Glu Glu
97          530                 535                 540
98  Glu Asp Val His Tyr Glu Gln Val Arg Ala Arg Leu Ser Lys Arg Glu
99  545                 550                 555                 560
100 Ala Ile Val Val Leu Ala Gly His Pro Val Val Phe Val Ser Ser Gly
101                 565                 570                 575
102 Asn Glu Asn Leu Leu Leu Phe Ala Phe Gly Ile Asn Ala Gln Asn Asn
103             580                 585                 590
104 His Glu Asn Phe Leu Ala Gly Arg Glu Arg Asn Val Leu Gln Gln Ile
105         595                 600                 605
106 Glu Pro Gln Ala Met Glu Leu Ala Phe Ala Ala Pro Arg Lys Glu Val
```

```
        RAW SEQUENCE LISTING              DATE: 12/28/2000
        PATENT APPLICATION: US/09/331,631A      TIME: 08:00:58

          Input Set : A:\CULLN23SEQ.txt
          Output Set: N:\CRF3\12282000\I331631A.raw

107       610               615               620
108   Glu Glu Ser Phe Asn Ser Gln Asp Gln Ser Ile Phe Phe Pro Gly Pro
109   625               630               635               640
110   Arg Gln His Gln Gln Gln Ser Pro Arg Ser Thr Lys Glu Gln Gln Pro
111                     645               650               655
112   Leu Val Ser Ile Leu Asp Phe Val Gly Phe
113                     660               665
115   <210> SEQ ID NO: 2
116   <211> LENGTH: 2171
117   <212> TYPE: DNA
118   <213> ORGANISM: Macadamia integrifolia
120   <220> FEATURE:
121   <221> NAME/KEY: sig_peptide
122   <222> LOCATION: (1)...(85)
124   <221> NAME/KEY: mat_peptide
125   <222> LOCATION: (86)...(1999)
127   <400> SEQUENCE: 2
128   atggcgatca atacatcaaa tttatgttct cttctctttc tccttcact  cttccttctg     60
129   tctacgacag tgtctcttgc tgaaagtgaa tttgacaggc aggaatatga ggagtgcaaa    120
130   cggcaatgca tgcagttgga gacatcaggc cagatccgtc ggtgtgtgag tcagtgcgat    180
131   aagagatttg aagaggatat agattggtct aagtatgata accaagagga tcctcagacg    240
132   gaatgccaac aatgccagag gcgatgcagu cagcaggaga gtggccacg  tcagcaacaa    300
133   tactgccaac gacgctgcaa ggaaatatgt gaagaagaag aagaatataa ccgacaacgt    360
134   gatccacagc agcaatacga gcaatgtcag aagcactgcc aacggcgcga gacagagcca    420
135   cgtcacatgc aaacatgtca acaacgctgc gagaggagat atgaaaagga gaaacgtaag    480
136   caacaaaaga gatatgaaga gcaacaacgt gaagacgaag agaaatatga agagcgaatg    540
137   aaggaagaag ataacaaacg cgatccacac aaagagagt  acgaagactg ccggaggcgc    600
138   tgcgaacaac aggagccacg tcagcagcac cagtgccagc taagatgccg agagcagcag    660
139   aggcaacacg gccgaggtgg cgatatgatg aaccctcaga ggggaggcag cggcagatac    720
140   gaggagggag aagaggagca aagcgacaac ccctactact tcgacgaacg aagcttaagt    780
141   acaaggttca ggaccgagga aggccacatc tcagttctgg agaacttcta tggtagatcc    840
142   aagcttctac gcgcactaaa aaactatcgc ttggtgctcc tcgaggctaa ccccaacgcc    900
143   ttcgtgctcc ctacccactt ggatgcagat gccattctct tggtcatagg agggagagga    960
144   gccctcaaaa tgatccacca cgacaacaga gaatcctaca acctcgagtg tggagacgta   1020
145   atcagaatcc cagctggaac cacattctac ttaatcaacc gagacaacaa cgagaggctc   1080
146   cacatagcca agttcttaca gacccatatcc actcctggcc aatacaagga attcttccca   1140
147   gctggaggcc aaaaccaga  gccgtacctc agtaccttca gcaaagagat tctccaggct   1200
148   gcgctcaaca cacaaacaga gaagctgcgt ggggtgtttg gacagcaaag ggaggggagtg   1260
149   ataattaggg cgtcacagga gcagatcagg gagttgactc gagatgactc agagtcacga   1320
150   cactggcata taaggagagg tggtgaatca agcaggggac cttacaatct gttcaacaaa   1380
151   aggccactgt actccatcaa atacggtcaa gcctacgaag tcaaacctga ggactacagg   1440
152   caactccaag acatggactt atcggttttc atagccaacg tcacccaggg atccatgatg   1500
153   ggtcccttct tcaacactag gtctacaaag gtggtagtgg tggctagtgg agaggcagat   1560
154   gtggaaatgg catgccctca cttgtcggga agacacggcg gccgcggtgg aggaaaaagg   1620
155   catgaggagg aagaggatgt gcactatgag caggttagag cacgtttgtc gaagagagag   1680
156   gccattgttg ttctggcagg tcatcccgtc gtcttcgttt catccggaaa cgagaacctg   1740
157   ctgctttttg catttggaat caatgcccaa aacaaccacg agaacttcct cgcggggaga   1800
158   gagaggaacg tgctgcagca gatagagcca caggcaatgg agctagcgtt tgccgctcca   1860
159   aggaaagagg tagaagagtc atttaacagc caggaccagt ctatcttctt tcctgggccc   1920
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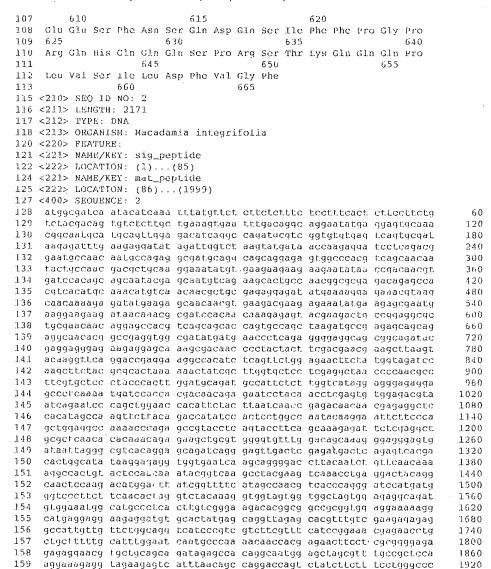
RAW SEQUENCE LISTING   DATE: 12/28/2000
PATENT APPLICATION: US/09/331,631A   TIME: 08:00:58

Input Set : A:\CULLN23SEQ.txt
Output Set: N:\CRF3\12282000\I331631A.raw

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160  aggcagcacc agcaacagtc gcccgctcc accaagcaac aacagcctct cgtctccatt   1980
161  ctggacttcg ttggcttcta aagttccaca aaaaagagtg tgttatgtag tataggttag   2040
162  tagctcctag ctcggtgtat gagagtagta agactaag acgctaaatc cctaagtaac    2100
163  taacctggcg agcttgcgtg tatgcaaata aagaggaaca gctttccaac tttaaaaaaa   2160
164  aaaaaaaaaa a                                                        2171
166  <210> SEQ ID NO: 3
167  <211> LENGTH: 666
168  <212> TYPE: PRT
169  <213> ORGANISM: Macadamia integrifolia
171  <220> FEATURE:
172  <221> NAME/KEY: SIGNAL
173  <222> LOCATION: (1)...(28)
175  <221> NAME/KEY: PEPTIDE
176  <222> LOCATION: (29)...(666)
178  <400> SEQUENCE: 3
179  Met Ala Ile Asn Thr Ser Asn Leu Cys Ser Leu Leu Phe Leu Leu Ser
180  1               5                   10                  15
181  Leu Phe Leu Leu Ser Thr Thr Val Ser Leu Ala Glu Ser Glu Phe Asp
182                  20                  25                  30
183  Arg Gln Glu Tyr Glu Glu Cys Lys Arg Gln Cys Met Gln Leu Glu Thr
184          35                  40                  45
185  Ser Gly Gln Met Arg Arg Cys Val Ser Gln Cys Asp Lys Arg Phe Glu
186      50                  55                  60
187  Glu Asp Ile Asp Trp Ser Lys Tyr Asp Asn Asp Asp Pro Gln Thr
188  65                  70                  75                  80
189  Asp Cys Gln Gln Cys Gln Arg Arg Cys Arg Gln Glu Ser Gly Pro
190                  85                  90                  95
191  Arg Gln Gln Gln Tyr Cys Gln Arg Arg Cys Lys Glu Ile Cys Glu Glu
192              100                 105                 110
193  Glu Glu Glu Tyr Asn Arg Gln Arg Asp Pro Gln Gln Gln Tyr Glu Gln
194          115                 120                 125
195  Cys Gln Glu Arg Cys Gln Arg His Glu Thr Gly Pro Arg His Met Gln
196      130                 135                 140
197  Thr Cys Gln Gln Arg Cys Glu Arg Arg Tyr Glu Lys Glu Lys Arg Lys
198  145                 150                 155                 160
199  Gln Gln Lys Arg Tyr Glu Glu Gln Gln Arg Glu Asp Glu Glu Lys Tyr
200                  165                 170                 175
201  Glu Glu Arg Met Lys Glu Glu Asp Asn Lys Arg Asp Pro Gln Gln Arg
202              180                 185                 190
203  Glu Tyr Glu Asp Cys Arg Arg Arg Cys Glu Gln Gln Glu Pro Arg Gln
204          195                 200                 205
205  Gln Tyr Gln Cys Gln Arg Arg Cys Arg Glu Gln Gln Arg Gln His Gly
206      210                 215                 220
207  Arg Gly Gly Asp Leu Ile Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr
208  225                 230                 235                 240
209  Glu Glu Gly Glu Glu Lys Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu
210                  245                 250                 255
211  Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val
212                  260                 265                 270
```

```
213   Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn
214           275                 280                 285
215   Tyr Arg Leu Val Leu Leu Glu Ala Asn Pro Asn Ala Phe Val Leu Pro
216           290                 295                 300
217   Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Thr Gly Gly Arg Gly
218   305                 310                 315                 320
219   Ala Leu Lys Met Ile His Arg Asp Asn Arg Glu Ser Tyr Asn Leu Glu
220                 325                 330                 335
221   Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile
222           340                 345                 350
223   Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr
224           355                 360                 365
225   Ile Ser Thr Pro Gly Gln Tyr Lys Glu Phe Phe Pro Ala Gly Gly Gln
226           370                 375                 380
227   Asn Pro Glu Pro Tyr Leu Ser Thr Phe Ser Lys Glu Ile Leu Glu Ala
228   385                 390                 395                 400
229   Ala Leu Asn Thr Gln Ala Glu Arg Leu Arg Gly Val Leu Gly Gln Gln
230                 405                 410                 415
231   Arg Glu Gly Val Ile Ile Ser Ala Ser Gln Glu Gln Ile Arg Glu Leu
232           420                 425                 430
233   Thr Arg Asp Asp Ser Glu Ser Arg Arg Trp His Ile Arg Arg Gly Gly
234           435                 440                 445
235   Glu Ser Ser Arg Gly Pro Tyr Asn Leu Phe Asn Lys Arg Pro Leu Tyr
236           450                 455                 460
237   Ser Asn Lys Tyr Gly Gln Ala Tyr Glu Val Lys Pro Glu Asp Tyr Arg
238   465                 470                 475                 480
239   Gln Leu Gln Asp Met Asp Val Ser Val Phe Ile Ala Asn Ile Thr Gln
240                 485                 490                 495
241   Gly Ser Met Met Gly Pro Phe Phe Asn Thr Arg Ser Thr Lys Val Val
242                 500                 505                 510
243   Val Val Ala Ser Gly Glu Ala Asp Val Glu Met Ala Cys Pro His Leu
244           515                 520                 525
245   Ser Gly Arg His Gly Gly Arg Arg Gly Gly Lys Arg His Glu Glu Glu
246           530                 535                 540
247   Glu Asp Val His Tyr Glu Gln Val Lys Ala Arg Leu Ser Lys Arg Glu
248   545                 550                 555                 560
249   Ala Ile Val Val Pro Val Gly His Pro Val Val Phe Val Ser Ser Gly
250                 565                 570                 575
251   Asn Glu Asn Leu Leu Leu Phe Ala Phe Gly Ile Asn Ala Gln Asn Asn
252           580                 585                 590
253   His Glu Asn Phe Leu Ala Gly Arg Glu Arg Asn Val Leu Gln Gln Ile
254           595                 600                 605
255   Glu Pro Gln Ala Met Glu Leu Ala Phe Ala Ala Pro Arg Lys Glu Val
256   610                 615                 620
257   Glu Glu Leu Phe Asn Ser Gln Asp Glu Ser Ile Phe Phe Pro Gly Pro
258   625                 630                 635                 640
259   Arg Gln His Gln Gln Gln Ser Ser Arg Ser Thr Lys Gln Gln Gln Pro
260                 645                 650                 655
261   Leu Val Ser Ile Leu Asp Phe Val Gly Phe
```

PYI:

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which pres nts at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 12/28/2000
PATENT APPLICATION: US/09/331,631A   TIME: 08:00:59

Input Set : A:\CULLN23SEQ.txt
Output Set: N:\CRF3\12282000\I331631A.raw

```
L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1238 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1238 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1238 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:31
L:1240 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1240 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
M:340 Repeated in SeqNo=31
L:1253 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
L:1253 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
L:1253 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
L:1255 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
L:1255 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
M:340 Repeated in SeqNo=32
L:1268 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
L:1268 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
L:1268 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:33
L:1270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
L:1270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
M:340 Repeated in SeqNo=33
L:1284 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:1284 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:1284 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
L:1286 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:1286 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
M:340 Repeated in SeqNo=34
L:1300 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:1300 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
L:1300 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:35
L:1302 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:1302 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
M:340 Repeated in SeqNo=35
L:1316 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
L:1316 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
L:1316 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
L:1318 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
L:1318 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
M:340 Repeated in SeqNo=36
L:1331 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:37
L:1331 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:37
L:1331 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:37
L:1333 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:37
L:1333 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:37
M:340 Repeated in SeqNo=37
L:1346 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:38
L:1346 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
L:1346 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38
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VERIFICATION SUMMARY   DATE: 12/28/2000
PATENT APPLICATION: US/09/331,631A   TIME: 08:00:59

Input Set : A:\CULLN23SEQ.txt
Output Set: N:\CRF3\12282000\I331631A.raw

L:1348 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:38
L:1348 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
M:340 Repeated in SeqNo=38
L:1361 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:39
L:1361 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:39
L:1361 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:39
L:1363 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:39
L:1363 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:39
M:340 Repeated in SeqNo=39
L:1376 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:40
L:1376 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:40
L:1376 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40